

# Modeling the Purkinje Conduction System with a Non Deterministic Rule Based Iterative Method

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## Abstract

*A method to construct a Purkinje system automatically for a particular subject is presented. The system is grown using a rule-based algorithm controlled by stochastic and probabilistic decisions that determine the particular structure of the model. A set of user customizable parameters control the final structure, and allow obtaining realistic Purkinje structures. The construction of the whole structure takes less than 30 s in a 2.4 GHz PC. The Purkinje system is built on a ventricular surface mesh previously obtained by segmentation. Geometrically, the system is modeled as a set of lines organized in a tree-like structure, so it can be included in a cardiac electrophysiological solver as a set of cables using a 1D type resolution method. The Purkinje systems obtained closely resemble real photographs and histological diagrams as for example Tawara and Myorburg ones.*

## 1. Introduction

The specialized electrical cardiac conduction system (CCS) coordinates the excitation and consequently the contraction of the ventricles. The electrical impulse, initiated in the sino-atrial node, reaches the His-bundle and rapidly propagates through the whole Purkinje system. Then, the electrical impulse enters the myocardium through the Purkinje-myocardium junctions (PMJ) distributed throughout the ventricular subendocardium. Therefore, including the His-Purkinje system in a computational model of the heart is fundamental to obtain realistic electrophysiological simulations. The CCS was well characterized by Tawara in 1906 [1], who described the atrioventricular (AV) conduction axis. Nonetheless there is still a lot of controversy about its origin, development and morphology. Despite the advances on medical imaging that allow the construction of accurate cardiac models [2], the reconstruction of the CCS has remained largely elusive. As a consequence, and due to the lack of

detailed in-vivo information, specially from distal areas, the CCS is often not included, or included using simplistic models [3–5] in computer cardiac modelling. However, its presence in realistic models is mandatory in order to obtain meaningful simulations of heart electrophysiology and electro-mechanics, as for example to study cardiac arrhythmias or electrical therapies such as Cardiac Resynchronization Therapy (CRT). In CRT, the cardiac response is highly dependent on the distal CCS retrograde activation, which cannot be simulated without a proper Purkinje system [6].

In this study we present a procedure to automatically build the atrio-ventricular section of the CCS on a 3D ventricular model. The system generated is composed of a set of 1D structures that represent the Purkinje fibers. These fibers are grown on the endocardial surface following a set of rules, similar to those used on L-systems [7], enhanced with non-deterministic decisions. The fibers start at the end of the bundle branches, ramify over the apical region and extend out towards anterior, posterior and free walls of the ventricles. The growing rules determine the characteristics of the structure produced, such as the overall density of branches and terminals. The complete structure is built in two steps, first the backbone of the network that spreads over the ventricles with little branch density, and second the smaller terminal branches that connect to the myocardial tissue. The growing method is flexible enough to produce a great variety of Purkinje tree structures. The methodology described here might help in the inclusion of a Purkinje system into a computer model and improve the realism of electrophysiology simulations.

## 2. Anatomical model construction

In this study, the Purkinje trees are grown on a geometrical surface mesh that represents a normal left ventricle (LV). This mesh, made of triangular elements, was built from a previously segmented computer tomography scan image [8] using an atlas based technique [2]. The advantage of using an atlas based technique, is that en-

docardium and epicardium regions, together with a set of other anatomical landmarks can be automatically labelled on the segmented surfaces. These labels are needed for the construction of the CCS.

The algorithm implemented, initiates the ramifications of the Purkinje tree at the end of the bundle branches, so the His and bundle branches must be previously included in the surface mesh. This procedure enables the use of different initial structures to simulate specific morphological observations. For this study, the His plus bundle branch model used contains two ramifications close to the insertion of the papillary muscles (see Fig. 1). This model was included in the surface mesh, fitting the structure to the septal wall of the left ventricle (LV) with a geometrical affine transformation.

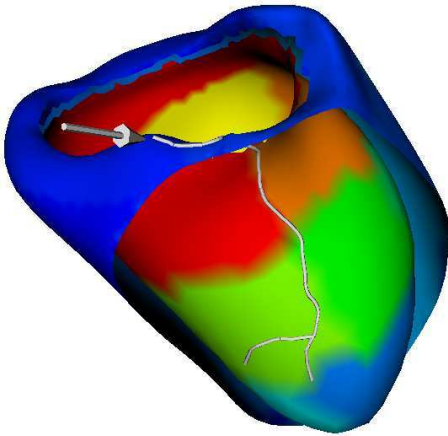


Figure 1. **Left ventricle model.** Model automatically segmented from a CT scan of a healthy human subject. Colors represent the 17 segment division from AHA. The white wire is included in the model as the proximal section of the atrio-ventricular conduction system. The arrow indicated the approximate position of the AV node in the model.

### 3. Growing algorithm

The process for building the Purkinje network is based on production rules similar to the ones used on L-systems [7]. Fig.2 displays the two types of rules used for the generation of a Purkinje network: in every time step two new branches separated by an angle  $\alpha$  are appended to every branch end. When using the rule ‘Y’ (see Fig.2 (a)), the new branches grow symmetrically in opposite directions, while in the case of rule ‘L’ (see Fig.2 (b)), one of the new branches preserves the original direction. Rule ‘L’ leads

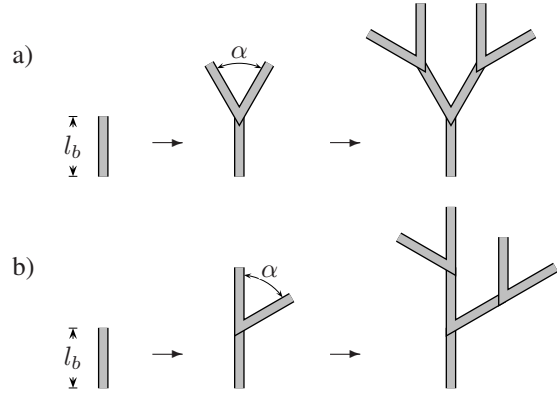


Figure 2. **Production rules.** Two new branches separated by an angle  $\alpha$  are added to every branch end. a) the new branches grow symmetrically in opposite directions; b) one of the new branches preserves the original direction.

to tree-like configurations, with main branches that ramify into child branches. The branch that maintains the previous direction is randomly chosen.

Loops are not allowed in the network. The branches stop growing just before crossing other already existent branches or when coming closer to other branches. They also stop growing when they reach the basal region.

In order to include non-deterministic characteristics to the system, the values of the length of the branches ( $l_b$ ) and the separation angle ( $\alpha$ ) are chosen for every branch following a normal distributions with means  $l_b$  and  $\alpha$ , and with standard deviations  $\sigma_l$  and  $\sigma_\alpha$ , respectively. Moreover, every branch is composed of  $N$  smaller segments that follow the established mainstream direction of the branch, but with smooth changes of angle between consecutive segments. This leads to more realistic curved branches instead of straight ones (see Fig.3). The new direction of every segment in a branch is decided by trying to keep distant to the existent surrounding branches in the network. The curvature of the branches is limited by a weighting parameter and by a maximum angle to avoid spiral-like branches.

All the parameters mentioned, as well as the growing

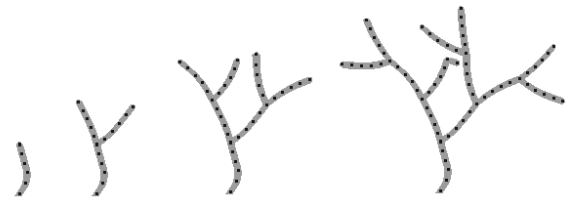


Figure 3. **Branches development.** Example of the production rule applied to curved branches made of  $N = 5$  segments.

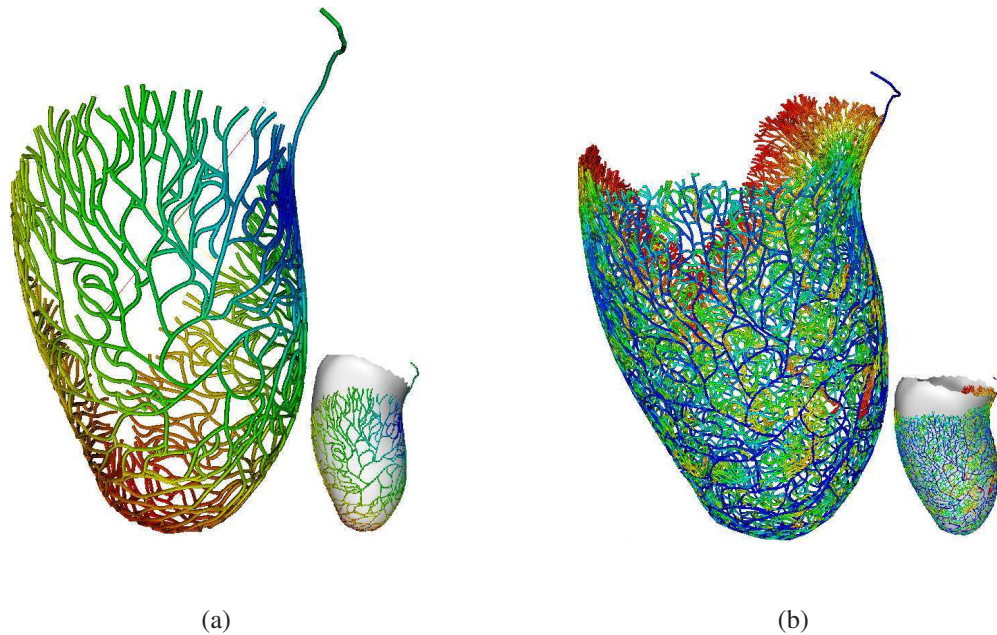


Figure 4. **Purkinje network.** Automatic construction of a Purkinje network on a segmented human endocardial surface mesh. (a) backbone of the Purkinje network and (b) terminal section and PMJs.

rule, i.e., ‘Y’ or ‘L’, are defined as input values for the algorithm. The network is generated in a 3D space, following the geometry of the LV endocardial surface mesh. After deciding the direction and length of every segment, they are projected over the mesh. The final network consists of a mesh made of line elements. The code was written in C++ using the VTK 5.2.1 (The Visualization Toolkit) library.

The algorithm builds the Purkinje tree in two consecutive steps. First, the main branches that constitute a “backbone network” expand over the endocardium growing towards the apex and back to basal regions. Then, the terminal branches and PMJs are appended along the main branches, developing smaller structures.

**Backbone network.** The construction of the “backbone network” starts at the end of the bundle branches. The algorithm starts applying the chosen production rule in an iterative way, to generate the main branches (see Fig. 4a). The backbone stops growing when the network has a certain number of branches or when there are no branches where the rule can be applied. This last condition occurs when all the branches stopped growing because they were about to cross other branches or because they were in the basal region.

**Terminal branches.** After growing the backbone, the number of subbranches that will grow from each main branch is calculated, i.e., none, one or two. Then, the pro-

duction rule is applied again in an iterative way to generate the terminal branches with a decreased mean branch length ( $l_b$ ). Since the PMJs are the only points of connection between the bulk myocardium and the Purkinje system a tight control on the density is desired (see Fig.4b). Short branches with few generations are produced along the backbone in order to reach desired local densities. Growing is limited by the space left by the initial backbone network.

#### 4. Electrophysiology modelling

Once the tree is constructed, the system can be used for computational simulations on cardiac electrophysiology. Depending on the package used for the simulations, the network is processed according to specific requirements. This processing includes refining the network to obtain a certain resolution, as for example around  $300 \mu\text{m}$  between nodes. It also includes separating the network in a set of branches, where every branch is composed of connected line segments without ramifications. Moreover, the terminal points in the network might need to be labelled in order to connect them to the ventricles volumetric mesh.

#### 5. Results and discussion

The algorithm described was used to generate Purkinje trees on a LV endocardial surface mesh of a patient with a

normal heart geometry. The trees generated resembled the intricate architecture observed in histological and morphological studies [9, 10]. The main structure, often visualized in animals using dyes, forms a polygonal pattern that extends over the endocardial surface (see Fig. 4a).

Building the CCS in two steps helped to produce different morphologies with similar densities. Using a backbone network with an average branch length of 6mm, which is around 30 times the real size, allowed to construct large branches and orientate the growing direction of the tree. Then, the subbranches with a reduced mean branch length grew randomly, filling the empty areas with the structures that contain the PMJs, but keeping the main network. The algorithm automatically searches for empty areas to grow the new branches, but always controlling the angles between consecutive branches. This results in a competitive process that leads to a natural broader expansion of the tree. Nonetheless, for highly dense trees a negative effect was obtained, since the branches curved to avoid neighbors, leading to many terminals close to the main branches.

The time required by the algorithm to build the tree structures is around 30 seconds in a 2.4 GHz PC, even when highly dense trees were produced. The use of an "L" rule instead of a "Y" rule, i.e. using a main direction to grow consecutive branches plus a bifurcation, produced better results for the backbone network, since it was easier to cover the endocardial surface and avoid death-loops between branches.

## 6. Conclusions

A method to build automatically a 3D Purkinje network for a particular subject was presented. The procedure is based on L-system type rules, and consists in two main steps: first the backbone of the network is built, and second the local smaller branches are generated. The method is controlled by ten parameters that allow to control the length of branches, the angles and the overall morphology of the tree. The growing procedure depends on the previous sections of the network already generated, since it takes into account the position of neighbor branches and competes for empty spaces, similar to the process of root growing in trees. One limitation of the algorithm is that the structure is loop-free, so it cannot produce exactly the same patterns observed in real Purkinje structures. In addition, the results might be improved if the parameters could be controlled locally. In that way, the local densities and local ramification would allow to produce more realistic trees and consequently more accurate activation maps.

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